OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on: May 27, 2005, 08:52:42 ; Search time 4551 Seconds
                    (without alignments)
                    3788.863 Million cell updates/sec

Title: US-10-054-534B-14
Perfect score: 2415
Sequence: 1 MVQGQKAEKISWATIREHNR...........EVVHLERISIEFFKEPPAM 453

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
             Maximum Match 100%
             Listing first 45 summaries

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext 0.5
               Ygapop 10.0 , Ygapext 0.5
               Fgapop 6.0 , Fgapext 7.0
               Delop 6.0 , Delext 7.0

Command line parameters:
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-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000000
-USER=US10054534 @CGN 1 1.3437 @runat_26052005 164253 18398 -NCBI=6 -ICPU=3
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-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   EST:*
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          3: gb_htc:*
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          5: gb_est4:*
          6: gb_est5:*
          7: gb_est6:*
          8: gb_gss1:*
          9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB#	ID	Description
1	571	23.6	1764	3	AY103762	AY103762 Zea mays
2	503.5	20.8	1569	3	CNS0ASSQ	BX824444 Arabidops
3	498.5	20.6	1335	9	AY418548	AY418548 Homo sapi
4	493	20.4	1335	9	AY418550	AY418550 Mus muscu
5	491	20.3	1658	9	CNS0A8LS	BX820915 Arabidops
6	486.5	20.1	1946	3	BC068224	BC068224 Danio rer
7	485.5	20.1	1521	3	CR611884	CR611884 full-leng
8	485.5	20.1	1530	3	CR597486	CR597486 full-leng
9	485.5	20.1	1641	3	CR591980	CR591980 full-leng

10	485.5	20.1	4213	3	HSM802921	AL512760 Homo sapi
11	482	20.0	3318	3	AX083959	AX083959 Mus muscu
12	481	19.9	1619	3	CNS0A7DY	BX823276 Arabidops
13	463.5	19.2	761	7	AK080414	CN200461 Tor10137
14	453.5	18.8	1689	3	AK080414	AK080414 Mus muscu
15	450.5	18.7	3129	3	AK029318	AK029318 Mus muscu
16	449.5	18.6	1690	3	CR608795	CR608795 full-leng
17	427	17.7	2862	3	AK083282	AK083282 Mus muscu
18	427	17.7	3697	3	AK090042	AK090042 Mus muscu
19	419.5	17.4	2272	3	AK076485	AK076485 Mus muscu
20	406.5	16.8	922	9	CG238209	CG238209 OGO82161
21	399	16.5	934	9	CG264599	CG264599 OGWGP72T
22	395	16.4	938	9	CG237761	CG237761 OGYBS48T
23	393.5	16.3	1131	3	AY420236	AY420236 OGYBS48T
24	392.5	16.2	1641	3	CR593148	CR593148 full-leng
25	390.5	16.2	1131	9	AY420234	AY420234 Homo sapi
26	383.5	15.9	886	9	CG440392	CG440392 OGTBY94T
27	378	15.7	914	9	CG463170	CG463170 OGTBY94T
28	369.5	15.3	1079	9	AY420235	AY420235 PU1JP24T
29	367	15.2	1283	9	AY418549	AY418549 Pan trogl
30	363.5	15.1	829	7	CN202441	CN202441 Pan trogl
31	361.5	15.0	985	6	CB264523	CB264523 Tor2601 G
32	350	14.5	742	5	CV198376	CV198376 55-E02082
33	346	14.3	920	7	CV198376	CV198376 CGFL00397
34	345	14.3	884	5	CO118959	CO118959 GR Eb021
35	340	14.1	823	8	BQ881930	BQ881930 AGENCOURT
36	337.5	14.0	869	9	BH687867	BH687867 BOHSQ4WTP
37	335.5	13.9	2813	3	CG449172	CG449172 OG9AD87TH
38	334	13.8	786	6	AK033308	AK033308 Mus muscu
39	331	13.7	722	5	CD837141	CD837141 BN45.O51D
40	331	13.7	741	5	BU024653	BU024653 QHR5H12.y
41	331	13.7	741	5	BU028011	BU028011 QHG9G05.y
42	330	13.7	821	7	BU025031	BU025031 QHF7E24.y
43	330	13.7	1509	3	CO129755	CO129755 GR Eb31C
44	329	13.6	702	5	CR618275	CR618275 full-leng
45	328	13.6	736	5	BU025987	BU025987 QHG12U15.

ALIGNMENTS

RESULT 1
AY103762

LOCUS   AY103762   1764 bp   mRNA   linear   HTC 16-OCT-2002
DEFINITION   Zea mays PCO087385 mRNA sequence.
ACCESSION   AY103762
VERSION   AY103762.1   GI:21206840
KEYWORDS   HTC.
SOURCE   Zea mays
  ORGANISM   Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 1764)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
          Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE   Maize Mapping Project/DuPont Consensus Sequences for Design of
          Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2 (bases 1 to 1764)
  AUTHORS   Coe,E.H.
  TITLE   Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
          Missouri, Columbia, MO 65211, USA
COMMENT   If you are interested in getting corresponding physical clones,
          these are publicly available from ZmDB and may be found by BLAST
          searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
          www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
          maize cDNA sequences is either Virginia Walbot, Stanford or Pat
          Schnable, Iowa State, then clones may be requested from ZmDB.
          www.zmdb.iastate.edu.
FEATURES   Location/Qualifiers
  source   1..1764
          /organism="Zea mays"

OM protein - nucleic search, using frame_plus_p2n model

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GenCore version 5.1.6

Run on: May 27, 2005, 09:16:26 ; Search time 816 Seconds
                 (without alignments)
                 3408.358 Million cell updates/sec

Title: US-10-054-534B-14
Perfect score: 2415
Sequence: 1 MVQGQKAEKISWATIREHNR.........EVVHLERISIEFFKEFPAM 453

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop   6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 5700845 seqs, 3069779757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-FGAPOP=6 -FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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                 4: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/US0A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2415	100.0	1362	10	US-09-769-863-13	Sequence 13, Appl
2	2415	100.0	1362	16	US-10-054-534B-13	Sequence 13, Appl
3	2415	100.0	1362	16	US-10-431-952-13	Sequence 13, Appl
4	2415	100.0	1362	18	US-10-776-311-35	Sequence 35, Appl
5	1537	63.6	1380	9	US-09-967-477B-7	Sequence 7, Appll
6	1129.5	46.8	1434	17	US-10-250-821-3	Sequence 3, Appli
7	1129.5	46.8	1434	17	US-10-278-391-3	Sequence 3, Appli
8	943	39.0	1374	16	US-10-840-478-1	Sequence 1, Appli
9	943	39.0	1374	18	US-10-840-478-25	Sequence 25, Appl
10	943	39.0	1374	18	US-10-840-325-36	Sequence 36, Appl
11	943	39.0	1374	18	US-10-840-325-129	Sequence 129, App
12	943	39.0	1617	18	US-10-776-311-33	Sequence 33, Appl
13	943	39.0	10328	19	US-10-250-821-28	Sequence 28, Appl
14	922.5	38.2	8894	19	US-10-840-325-124	Sequence 124, App
15	758	31.4	1578	17	US-10-250-821-7	Sequence 7, Appli
16	758	31.4	1578	17	US-10-250-553-7	Sequence 7, Appli
17	758	31.4	15430	17	US-10-250-821-25	Sequence 25, Appl
18	758	31.4	15430	17	US-10-250-553-25	Sequence 25, Appl
19	758	31.4	17752	17	US-10-250-821-28	Sequence 28, Appl
20	758	31.4	17752	17	US-10-250-553-28	Sequence 28, Appl
21	570.5	23.6	1944	18	US-10-437-963-83761	Sequence 83761, A
22	565.5	23.4	2144	17	US-10-425-114-15122	Sequence 15122, A
23	565.5	23.4	2356	17	US-10-424-599-56986	Sequence 56986, A
24	565	23.4	2054	17	US-10-389-566-288	Sequence 288, App
25	561.5	23.3	1344	16	US-10-340-779A-2	Sequence 2, Appli
26	557.5	23.1	648	17	US-10-250-821-18	Sequence 18, Appl
27	557.5	23.1	648	17	US-10-250-553-18	Sequence 18, Appl
28	551	22.8	2236	17	US-10-424-599-124471	Sequence 124471,
29	547	22.7	1967	17	US-10-425-114-14991	Sequence 14991, A
30	535	22.2	1702	13	US-10-029-756-26	Sequence 26, Appl
31	535	22.2	1702	13	US-10-702-777-26	Sequence 26, Appl
32	528.5	21.9	1685	13	US-10-029-756-4	Sequence 4, Appli
33	528.5	21.9	1685	17	US-10-702-777-4	Sequence 4, Appll
34	522.5	21.6	1350	9	US-09-938-842A-558	Sequence 558, App
35	522.5	21.6	1350	11	US-09-938-842A-558	Sequence 558, App
36	522.5	21.6	1828	17	US-10-425-114-14869	Sequence 14869, A
37	522.5	21.6	1883	18	US-10-739-930-3353	Sequence 3353, Ap
38	522.5	21.6	1940	17	US-10-424-599-36789	Sequence 36789, A
39	513.5	21.3	1302	18	US-10-437-963-83759	Sequence 83759, A
40	512.5	21.2	1302	19	US-10-504-424-3	Sequence 3, Appli
41	510.5	21.2	1503	18	US-10-767-795-879	Sequence 879, Appl
42	500.5	20.7	1362	19	US-10-504-424-1	Sequence 1, Appli
43	498.5	20.6	1362	17	US-10-239-652A-4	Sequence 4, Appli
44	498.5	20.6	3016	17	US-10-429-160-25	Sequence 25, Appli
45	498.5	20.6	3149	17	US-10-172-118-1010	Sequence 1010, Ap

ALIGNMENTS

RESULT 1
US-09-769-863-13

; Sequence 13, Application US/09769863
; Publication No. US20030157144A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.01
; CURRENT APPLICATION NUMBER: US/09/769,863
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1362
; TYPE: DNA

OM protein - nucleic search, using frame_plus_p2n model

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Run on: May 27, 2005, 08:55:06 ; Search time 249 Seconds
                 (without alignments)
                 2976.841 Million cell updates/sec

Title: US-10-054-534B-14
Perfect score: 2415
Sequence: 1 MVQGQKAEKISWATIREHNR.........EVVHLERISIEFFKEFPAM 453

Scoring table: BLOSUM62
                 Xgapop 10.0 ; Xgapext 0.5
                 Ygapop 10.0 ; Ygapext 0.5
                 Fgapop 6.0 ; Fgapext 7.0
                 Delop   6.0 ; Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10054534/runat_26052005_164253_18411/app_query.fasta_1.647
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	DB ID	Description
1	2415	100.0	1362	4	US-09-769-863-13	Sequence 13, Appl
2	943	39.0	1617	4	US-08-834-655-1	Sequence 1, Appli
3	943	39.0	1617	2	US-08-834-033A-1	Sequence 1, Appli
4	943	39.0	1617	3	US-09-363-574-1	Sequence 1, Appli
5	943	39.0	1617	3	US-09-363-526-1	Sequence 1, Appli
6	943	39.0	1617	3	US-09-330-235-17	Sequence 17, Appl
7	644.5	26.7	1281	4	US-09-857-583B-3	Sequence 3, Appli
8	561.5	23.3	1461	4	US-09-857-583B-1	Sequence 1, Appli
9	535	22.2	1702	3	US-08-934-254-26	Sequence 26, Appl
10	535	22.2	1702	4	US-09-685-775-26	Sequence 26, Appl
11	528.5	21.9	1684	4	US-08-831-570-1	Sequence 1, Appli
12	528.5	21.9	1684	2	US-08-831-575-1	Sequence 1, Appli

13	528.5	21.9	1685	1	US-08-366-779-4	Sequence 4, Appli
14	528.5	21.9	1685	1	US-08-789-936-4	Sequence 4, Appli
15	528.5	21.9	1685	3	US-08-934-254-4	Sequence 4, Appli
16	528.5	21.9	1685	4	US-09-685-775-4	Sequence 4, Appli
17	498.5	20.6	3158	4	US-09-949-016-4613	Sequence 4613, Ap
18	489.5	20.3	2257	3	US-09-439-261-8	Sequence 8, Appli
19	489.5	20.3	2257	3	US-09-439-261-8	Sequence 8, Appli
20	487.5	20.2	1335	4	US-09-439-261-1	Sequence 1, Appli
21	487.5	20.2	1335	3	US-09-227-613-1	Sequence 1, Appli
22	487.5	20.2	1335	3	US-09-227-613-1	Sequence 1, Appli
23	485.5	20.1	1928	3	US-09-048-888-2	Sequence 2, Appli
24	449.5	18.6	1717	4	US-09-016-4904	Sequence 4904, Ap
25	449.5	18.6	1758	4	US-09-949-016-4904	Sequence 4904, Ap
26	364	15.1	1320	4	US-09-769-863-28	Sequence 28, Appl
27	342	14.2	1843	3	US-09-227-613-7	Sequence 7, Appli
28	342	14.2	1843	3	US-09-227-613-7	Sequence 7, Appli
29	335	13.9	1413	4	US-09-769-863-19	Sequence 19, Appl
30	323.5	13.4	864	3	US-09-439-261-12	Sequence 12, Appl
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32	312	12.9	990	3	US-09-439-261-35	Sequence 35, Appl
33	312	12.9	990	3	US-09-227-613-34	Sequence 34, Appl
34	304	12.6	918	3	US-09-439-261-5	Sequence 5, Appli
35	304	12.6	918	3	US-09-227-613-5	Sequence 5, Appli
36	303	12.5	960	3	US-09-439-261-36	Sequence 36, Appl
37	303	12.5	960	3	US-09-227-613-35	Sequence 35, Appl
38	295	12.2	1478	4	US-09-148-545-63	Sequence 63, Appl
39	286.5	11.9	1483	4	US-09-227-613-35	Sequence 35, Appl
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41	284	11.8	1686	4	US-09-377-452-1	Sequence 1, Appli
42	284	11.8	1686	3	US-09-439-261-6	Sequence 6, Appli
43	241	10.0	2016	4	US-09-227-613-6	Sequence 6, Appli
44	237	9.8	1884	4	US-09-148-545-119	Sequence 119, App
45	237	9.8	1884	1	US-08-307-382-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1
US-09-769-863-13

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; Patent NO. 6635451
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.O1
; CURRENT APPLICATION NUMBER: US/09/769,863
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Saprolegnia diclina
; US-09-769-863-13

Alignment Scores:
Pred. No.:   1.77e-299
Score: 2415.00   Length: 1362
Percent Similarity: 100.00%   Matches: 453
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 4   Indels: 0
                                         Gaps: 0

US-10-054-534B-14 (1-453) x US-09-769-863-13 (1-1362)

Qy   1 MetValGlnGlyGlnLysAlaGluLysAlaSerTrpAlaThrIleArgGluHisAsnArg 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGTTCAGGGGCAAAAAGGCGGAGAAGATCTCGTGGGGCGACCATCCGTGAGCACAACGC 60

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on: May 27, 2005, 08:48:31 ; Search time 759 Seconds
                 3533.126 Million cell updates/sec

Title: US-10-054-534B-14
Perfect score: 2415
Sequence: 1 MVQCQKAEKISWAIIREHNR.........EVVVHLERISIEPFKEFPAM 453

Scoring table: BLOSUM62
                 Xgapop   10.0 , Xgapext   0.5
                 Ygapop   10.0 , Ygapext   0.5
                 Fgapop   6.0   , Fgapext   7.0
                 Delop   6.0   , Delext   7.0

Searched: 4390206 seqs, 295970667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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 -DB=N Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_16Dec04:*
             1: geneseqn1980s:*
             2: geneseqn1990s:*
             3: geneseqn2000s:*
             4: geneseqn2001as:*
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             6: geneseqn2002as:*
             7: geneseqn2002bs:*
             8: geneseqn2003as:*
             9: geneseqn2003bs:*
            10: geneseqn2003cs:*
            11: geneseqn2004as:*
            12: geneseqn2004aas:*
            13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2415	100.0	1362	8	AAD49064	Saprolegn
2	2415	100.0	1362	13	ADR20162	Saprolegn
3	1537	63.6	1380	6	AAD35090	Pythium i
4	1129.5	46.8	1434	6	ABV74258	Phaeodact
5	1129.5	46.8	1434	6	ABQ76780	P. tricor

6	1129.5	46.8	1443	13	ADR49337	Phaeodact
7	1129.5	46.8	17061	13	ADR49339	Plasmid P
8	943	39.0	1374	3	AAZ47129	Fungal de
9	943	39.0	1374	5	AAF25234	Nucleotid
10	943	39.0	1617	2	AAV63624	cDNA enco
11	943	39.0	1617	2	AAX00889	Mortierel
12	943	39.0	1617	2	AAA09430	M. alpina
13	943	39.0	1617	12	ADF89958	M. alpina
14	943	39.0	1404	8	ADR20160	Mortierel
15	818	33.9	1404	4	ABV76916	Nucleotid
16	817	33.8	2160	4	AAF25734	Physcomit
17	798.5	33.1	1467	4	AAF25730	C. purpur
18	798.5	33.1	2040	4	AAF25729	C. purpur
19	758	31.4	1578	6	ABV74260	Physcomit
20	758	31.4	1578	6	ABQ76782	P. patens
21	758	31.4	1578	13	ADR49314	Physcomit
22	758	31.4	2012	6	AAF26040	P. patens
23	758	31.4	2012	8	ABX13450	P. patens
24	758	31.4	2012	6	ABX13450	Plant spe
25	758	31.4	15430	6	ABQ76796	pB-DHG1A
26	758	31.4	15430	6	ABV74275	Plant spe
27	758	31.4	17752	6	ABQ76797	pBARA1 en
28	758	31.4	17752	13	ADR49324	P. tricor
29	631.5	26.1	1266	12	ADP87980	Euglena g
30	613	25.4	1275	2	AAS51233	B. gracil
31	588.5	24.4	1463	2	AAX76589	Caenorhab
32	571	23.6	1764	3	AAD01350	Corn sphi
33	565	23.4	2054	12	ADJ48284	Maize oil
34	561.5	23.3	1344	2	AAX86961	C. elegan
35	561.5	23.3	1344	8	ABX13451	C. elegan
36	561.5	23.3	1344	12	ADP87986	Ceratodon
37	561.5	23.3	1344	12	AAS51232	C. elegan
38	558.5	23.1	1606	3	AAZ44851	Sphingoli
39	558.5	23.1	648	8	ABV74268	Phaeodact
40	557.5	23.1	648	6	ABQ76790	P. tricor
41	550	22.8	1972	3	AAD01353	Wheat sph
42	535.5	22.2	1696	12	ADO15558	Evening p
43	535	22.2	1696	12	ADO15558	Evening p
44	535	22.2	1702	6	ABK49503	DNA encod
45	535	22.2	1702	8	ABX15367	Evening P
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ALIGNMENTS

RESULT 1
AAD49064
ID   AAD49064 standard; DNA; 1362 BP.
XX
AC   AAD49064;
XX
DT   07-MAR-2003 (first entry)
XX
DE   Saprolegnia diclina delta 6 desaturase DNA.
XX
KW   Delta 5 desaturase; delta 6 desaturase; polyunsaturated fatty acid; PUFA;
KW   angioplasty; osteoporosis; inflammation; rheumatoid arthritis; psoriasis;
KW   premenstrual syndrome; myalgic encephalitis; chronic fatigue; vasotropic;
KW   acquired immune deficiency syndrome; AIDS; multiple sclerosis; virucide;
KW   osteopathic; litholytic; nephrotropic; neuroprotective; anticoagulant;
KW   therapy; antilipaemic; hypotensive; kidney stone; cachexia; cytostatic;
KW   eczema; cancer; asthma; enzyme; gene; ds.
OS   Saprolegnia diclina.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..1362
FT   /*tag= a
FT   /product= "Saprolegnia diclina delta 6 desaturase"
XX
PN   WO200281668-A2.
XX
PD   17-OCT-2002.
XX

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on: May 27, 2005, 08:49:06 ; Search time 6201 Seconds
(without alignments)
3539.786 Million cell updates/sec

Title: US-10-054-534B-14
Perfect score: 2415
Sequence: 1 MVQGQKAEKISWATIREHNR.........EVVHLBRISIEFFKEFPAM 453

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop   6.0 , Delext   7.0

Searched: 4708233 seqs, 2422707955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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-DOCALIGN=200 -THR_SCORE=Pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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         2: gb_htg:*
         3: gb_in:*
         4: gb_om:*
         5: gb_ov:*
         6: gb_pat:*
         7: gb_ph:*
         8: gb_pl:*
         9: gb_pr:*
        10: gb_ro:*
        11: gb_rts:*
        12: gb_sy:*
        13: gb_un:*
        14: gb_vi:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	2415	100.0	1362	6	AX576988	AX576988 Sequence
3	1537	63.6	1380	8	AX467717	AX467717 Sequence
4	1537	63.6	1380	8	AF419296	AF419296 Pythium 1
5	1129.5	46.8	1434	6	AX481613	AX481613 Sequence
6	1129.5	46.8	1434	6	AX481942	AX481942 Sequence
7	1129.5	46.8	1434	6	AX951573	AX951573 Sequence
8	1129.5	46.8	1443	6	CQ874877	CQ874877 Sequence
9	1129.5	46.8	1669	8	AY082393	AY082393 Phaeodact
10	1129.5	46.8	17061	6	CQ874879	CQ874879 Sequence
11	944	39.1	1590	8	AB020032	AB020032 Mortierel
12	943	39.0	1374	6	BD232180	BD232180 Composit1
13	943	39.0	1374	6	AX951591	AX951591 Sequence
14	943	39.0	1374	6	AR080598	AR080598 Sequence
15	943	39.0	1617	6	AR098439	AR098439 Sequence
16	943	39.0	1617	6	AR136018	AR136018 Sequence
17	943	39.0	1617	6	AR215236	AR215236 Sequence
18	943	39.0	1617	6	AR235375	AR235375 Sequence
19	943	39.0	1617	6	BD082621	BD082621 Methods a
20	943	39.0	1617	6	BD092914	BD092914 Methods a
21	943	39.0	1617	6	AF110510	AF110510 Mortierel
22	940	38.9	1374	6	AF465282	AF465282 Mortierel
23	938	38.8	1374	6	AF306634	AF306634 Mortierel
24	932	38.6	1521	8	AB070555	AB070555 Mortierel
25	921	38.1	1521	8	AF465281	AF465281 Mortierel
26	917	38.0	1374	8	AF307940	AF307940 Mortierel
27	900	37.3	1482	8	AY320288	AY320288 Rhizopus
28	883	36.6	1743	8	AB070556	AB070556 Mortierel
29	856.5	35.5	2207	8	AB070557	AB070557 Mortierel
30	852	35.3	2175	8	AG601391	AG601391 Mortierel
31	829.5	34.3	1947	8	AF465283	AF465283 Mortierel
32	822.5	34.1	3175	8	AY583463	AY583463 Marchanti
33	818	33.9	1404	6	BD178222	BD178222 Fatty aci
34	818	33.9	1546	8	AB052086	AB052086 Mucor cir
35	817	33.8	1563	6	AF307940	AF307940 Mortierel
36	817	33.8	2160	6	AX058840	AX058840 Sequence
37	817	33.8	2160	6	AX058840	AX058840 Sequence
38	817	33.8	2160	6	AX951571	AX951571 Sequence
39	798.5	33.1	2160	6	AJ250735	AJ250735 Ceratodon
40	798.5	33.1	1467	6	AX058832	AX058832 Sequence
41	798.5	33.1	1467	6	AX951569	AX951569 Sequence
42	798.5	33.1	2040	6	AX058830	AX058830 Sequence
43	798.5	33.1	2040	8	AX951567	AX951567 Sequence
44	785.5	32.5	1071	8	AY621305	AY621305 Mortierel
45	783	32.4	1537	8	AY583316	AY583316 Rhizopus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
AR410195

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LOCUS       AR410195    1362 bp    DNA    linear    PAT 18-DEC-2003
DEFINITION  Sequence 13 from patent US 6635451.
ACCESSION   AR410195
VERSION     AR410195.1   GI:40161436
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1362)
  AUTHORS   Mukerji,P., Huang,Y.-S., Das,T., Thurmond,J. and Pereira,S.L.
  TITLE     Desaturase genes and uses thereof
  JOURNAL   Patent: US 6635451-A 13 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1..1362
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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Alignment Scores:
Pred. No.:	6.6e-232	Length: 1362
Score:	2415.00	Matches: 453
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	6	Gaps: 0

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: May 27, 2005, 05:35:03 ; Search time 388 Seconds
(without alignments)
597.866 Million cell updates/sec

Title: US-10-054-534B-14
Perfect score: 2415
Sequence: 1 MVQGQKAEKISWATIREHNR.........EVVVHLERISIEFFKEFPAM 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161237B seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 161237B

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   UniProt_03:*
1:   uniprot_sprot:*
2:   uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match Length	DB	ID	Description
1	1537	63.6	459	2	Q944W4	pythium irr
2	1129.5	46.8	477	2	Q8BXB0	phaedactyl
3	944	39.1	457	2	Q9UVY3	mortierella
4	943	39.0	457	2	Q9UVV3	mortierella
5	940	38.9	457	2	Q8X173	mortierella
6	938	38.8	457	2	Q9HEY4	mortierella
7	937	38.8	457	2	Q70BL2	mortierella
8	932	38.6	458	2	Q76LW8	mortierella
9	921	38.1	457	2	Q8X174	mortierella
10	917	38.0	457	2	Q9HEY1	mortierella
11	900	37.3	458	2	Q6PS62	rhizopus or
12	900	37.3	458	2	Q7Z8P2	rhizopus sp
13	822.5	34.1	481	2	Q96V8	marchantia
14	818	33.9	467	2	Q96VC3	mucor circi
15	818	33.9	467	2	Q6TMX2	mucor rouxi
16	817	33.8	520	2	Q9LEM9	ceratodon p
17	798.5	33.1	483	2	Q9LEN0	ceratodon p
18	785.5	32.5	357	2	Q6IV28	mortierella
19	779.5	32.3	357	2	Q9HDF4	mortierella
20	758	31.4	525	2	Q92NW2	physcomitre
21	613	25.4	419	2	Q9SWQ9	euglena gra
22	586.5	24.3	443	2	Q23221	caenorhabdi
23	585.5	24.2	443	2	O61388	caenorhabdi
24	570.5	23.6	466	2	Q6ERL2	oryza sativ
25	561.5	23.3	447	2	Q9XTB7	caenorhabdi
26	558.5	23.1	458	2	O43469	helianthus
27	558	23.1	446	2	Q8LD7	aquilegia v
28	549	22.7	469	2	Q9ZTU8	triticum ae
29	533.5	22.1	464	2	Q96V5	marchantia
30	533	22.1	446	2	Q7LBG5	anemone lev
31	532	22.0	446	2	Q7LBG4	anemone lev
32	530.5	22.0	448	2	Q8VZZ1	echium pita
33	529.5	21.9	448	2	Q8VZZ2	echium gent
34	528.5	21.9	448	2	Q9SAU5	borago offi
35	527.5	21.8	448	2	O04353	borago offi
36	523	21.7	446	2	Q92TY9	ricinus com
37	522.5	21.6	449	2	Q9ZRP7	arabidopsis
38	521.5	21.6	449	2	Q9ZRP8	brassica na
39	518.5	21.5	453	2	O81B96	arabidopsis
40	513.5	21.3	452	2	Q84KG6	primula via
41	509.5	21.1	452	2	Q84KG9	primula far
42	503	20.8	446	2	Q6DDK2	xenopus lae
43	502.5	20.8	452	2	Q84KG7	primula via
44	500.5	20.7	453	2	Q84KG8	primula far
45	500	20.7	444	1	FADS_BRARE	brachydanio

ALIGNMENTS

RESULT 1
Q944W4

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ID   Q944W4          PRELIMINARY;      PRT;    459 AA.
AC   Q944W4;
DT   01-DEC-2001 (TREMBLrel. 19, Created)
DT   01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE   Delta-6 fatty acid desaturase.
OS   Pythium irregulare.
OC   Eukaryota; Stramenopiles; Oomycetes; Pythiales; Pythiaceae; Pythium.
OX   NCBI_TaxID=36331;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hong H., Datta N., Mackenzie S.L., Qiu X.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the fatty acid desaturase family.
DR   EMBL; AF419296; AAL13310.1; -.
DR   HSSP; P04166; 1BSM.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR   InterPro; IPR008938; ARM.
DR   InterPro; IPR001199; Cyt_B5.
DR   InterPro; IPR005804; Fa_desat.
DR   InterPro; IPR012257; FA_desat_sub.
DR   Pfam; PF00173; Cyt-b5; 1.
DR   Pfam; PF00487; FA_desaturase; 1.
DR   ProDom; PD000612; Cyt_B5; 1.
DR   ProDom; PD001081; FA_desat_sub; 1.
DR   PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW   Fatty acid biosynthesis; Heme; Lipid synthesis; Oxidoreductase.
SQ   SEQUENCE 459 AA; 286464DA761BB055 CRC64;
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Query Match   63.6%;   Score 1537;   DB 2;   Length 459;
Best Local Similarity   62.8%;   Pred. No. 5e-124;
Matches 282;   Conservative 68;   Mismatches 93;   Indels 6;   Gaps 3;

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Qy   70 LLEQYYGDVDQSTAA--VDTSISDBVKKSQ---SDFIASYRKLRLEVRLGLYDSSKLY 124
         |||||||||| :||       ||  |:|     |: ||||:|||||||||| :::||
Db   72 LLEQFYGVDVDETSKARIBGEPASDERARRERINEFIASYRRLRVKVRKGMGLYDASALY 131

Qy  125 YLYKCASTLSIPALVSRAICLHFDSTAMYMVAAVILGLFYQQCGWLAHDFLHHQVFENHLP 184
         |:||||||| | | |  |  |||||||  |   ||| |||  |||||||||||||  ||||
Db  125 YAWKLVSTFGIAVLSMAICFFFNSFAMYMVAGVIMGLFYQQSGWLAHDFLHNQVCENRTL 191

Qy  185 GDLVGVMVGNLMQGFSVQWWKNKHNTHHAIPNLHATPEIAFHGDPDIDTMPILAWSLKMA 244
         |||||||||||||||||||||||||||||||:||||  :||||||||||||||||||| ||
Db  192 GNLIGCLVGNAWQGFSVQWWRNKHNLHHAVPNLHSAXDEGFIGDPDIDTMPLLAWSKEMA 251

Qy  245 QHAVDSPVGLFPMRYQAYLYFPILLFARISWVIQSAMYAFYNVGPGGTPDKYQYPLLRA 304
         |  |  |||| |::|| | |:    || :|| || |  |  |  |  | :|:  ||| |
```

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: May 27, 2005, 07:12:09 ; Search time 74 Seconds
(without alignments)
589.003 Million cell updates/sec

Scoring table: US-10-054-534B-14
Title: 2415
Perfect score:
Sequence: 1 MVQGQKAEKISWAPIREHNR..........EVVVHLERISIEFKEFPAM 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
PIR 79:*
1:   pir1:*
2:   pir2:*
3:   pir3:*
4:   pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	561.5	23.3	447	1	T43319	Delta5 fatty acid
3	558.5	23.1	458	1	S66358	Delta8 sphingolipi
4	548	22.7	454	2	H88791	protein T13F2.1 li
5	522.5	21.6	449	2	T47950	protein T13F2.1 li
6	521.5	21.6	449	2	T50555	delta-8 sphingolip
7	519.5	21.5	449	2	A84900	delta-8 sphingolip
8	498.5	20.6	444	2	T13155	hypothetical prote
9	487.5	20.2	444	2	JG0180	linoleoyl-CoA desa
10	456.5	18.9	523	2	JC7556	linoleoyl-CoA desa
11	399	16.5	345	2	T16617	probable Delta6 fa
12	237	9.8	359	2	S33157	Delta6 fatty acid
13	208	8.6	368	2	S54809	linoleoyl-CoA desa
14	195	8.1	134	2	T00796	cytochrome b5 At2g
15	189	7.8	139	2	S46306	cytochrome b5 - co
16	187	7.7	140	2	T52468	cytochrome b5 [imp
17	184.5	7.6	135	2	A86390	hypothetical prote
18	183	7.6	909	2	JN0665	nitrate reductase
19	182	7.5	120	2	S63052	cytochrome b5 - ye
20	181	7.5	911	1	RDTONH	nitrate reductase
21	180.5	7.5	135	2	S49200	cytochrome b5 - co
22	180	7.5	137	2	S46307	cytochrome b5 - ri
23	178	7.4	135	2	JC7671	ascidian cytochrom
24	171	7.1	889	2	T02240	nitrate reductase
25	167.5	6.9	135	2	T09946	cytochrome b5 - so
26	167	6.9	884	2	S66308	nitrate reductase
27	166.5	6.9	132	2	E84905	nitrate reductase
28	166.5	6.9	920	2	S52301	probable cytochrom
29	166	6.9	134	2	T14454	cytochrome b5 - wi
30	166	6.9	900	2	S47029	nitrate reductase
31	165.5	6.9	911	2	T08105	nitrate reductase
32	164.5	6.8	886	2	AS9223	nitrate reductase
33	164.5	6.8	891	1	RDBHNP	nitrate reductase
34	164.5	6.8	917	2	E96807	nitrate reductase
35	164.5	6.8	917	2	S35228	nitrate reductase
36	164	6.8	881	2	S25445	nitrate reductase
37	162	6.7	134	2	T52469	cytochrome b5 [imp
38	162	6.7	427	2	G70590	probable desA3 pro
39	162	6.7	916	2	S07554	probable nitrate reductase
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41	161.5	6.7	911	2	T08108	nitrate reductase
42	160.5	6.6	904	1	RDNTNS	nitrate reductase
43	159	6.6	890	2	T11805	nitrate reductase
44	158.5	6.6	898	1	RDBJNH	nitrate reductase
45	157.5	6.5	424	2	JC5891	omega 6 desaturase

ALIGNMENTS

RESULT 1
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linoleoyl-CoA desaturase (EC 1.14.19.3) W08D2.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
N;Alternate names: Delta6 fatty acid desaturase
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T26280; T37238
A;Accession: T26280; T37238
R;Swinburne, J.; Ainscough, R.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z20188
A;Experimental source: clone W08D2
R;Napier, J.A.; Hey, S.J.; Lacey, D.J.; Shewry, P.R.
Biochem. J. 330, 611-614, 1998
A;Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase by het
A;Reference number: Z21637; MUID:98149727; PMID:9480865
A;Residues: 1-473 <WIL>
A;Cross-references: UNIPROT:O61388; EMBL:Z70271; PIDN:CAA94233.1; GSPDB:GN00022; CESP:W
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A;Gene: CESP: W08D2.4
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A;Introns: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
C;Superfamily: fatty acid desaturase/sphingolipid desaturase
C;Keywords: alternative splicing; oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 23.5%; Score 567.5; DB 1; Length 473;
Best Local Similarity 30.3%; Pred. No. 1.8e-41;
Matches 146; Conservative 82; Mismatches 163; Indels 91; Gaps 15;

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Db   70 NSDATHIFHAFHEGSSQAYKQLDLLKKHGEHDBFLERKQLEKRLDKVDINVSAYDVSVAQR  129

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us-10-054-534b-14.rapb

OM protein - protein search, using sw model

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                GenCore version 5.1.6
                Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:         May 27, 2005, 08:47:10 ; Search time 468 Seconds
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Title:          US-10-054-534B-14
Perfect score:  2415
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Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2415	100.0	453	10	US-09-769-863-14	Sequence 14, Appl
2	2415	100.0	453	14	US-10-054-534B-14	Sequence 14, Appl
3	2415	100.0	453	14	US-10-431-952-14	Sequence 14, Appl
4	2415	100.0	453	16	US-10-776-311-36	Sequence 36, Appl
5	1537		459	9	US-09-967-477B-8	Sequence 8, Appli
6	1129.5	63.6	477	15	US-10-250-821-4	Sequence 4, Appli
7	1129.5	46.8	477	15	US-10-250-553-4	Sequence 4, Appli
8	1129.5	46.8	477	15	US-10-278-391-4	Sequence 4, Appli
9	943	39.0	457	16	US-10-776-311-34	Sequence 34, Appl
10	943	39.0	457	17	US-10-840-325-37	Sequence 37, Appl
11	943	39.0	458	11	US-10-191-513A-11	Sequence 11, Appl
12	943	39.0	458	14	US-10-191-513A-41	Sequence 41, Appl
13	758	31.4	525	15	US-10-250-821-8	Sequence 8, Appli
14	758	31.4	525	15	US-10-250-821-27	Sequence 27, Appl
15	758	31.4	525	15	US-10-250-821-30	Sequence 30, Appl
16	758	31.4	525	15	US-10-250-553-8	Sequence 8, Appli
17	758	31.4	525	15	US-10-250-553-27	Sequence 27, Appl
18	758	31.4	525	15	US-10-250-553-30	Sequence 30, Appl
19	713.5	29.5	323	14	US-10-191-513A-17	Sequence 17, Appl
20	593.5	24.6	443	14	US-10-340-779A-20	Sequence 20, Appl
21	570.5	23.6	466	15	US-10-437-963-186244	Sequence 186244,
22	567.5	23.5	473	15	US-10-369-493-6108	Sequence 6108, Ap
23	565.5	23.4	448	15	US-10-424-599-199828	Sequence 199828,
24	565.5	23.4	453	15	US-10-425-114-48669	Sequence 48669, A
25	565	23.4	515	15	US-10-389-566-447	Sequence 447, App
26	558.5	23.1	458	14	US-10-340-779A-11	Sequence 11, Appl
27	557.5	23.1	216	15	US-10-250-821-19	Sequence 19, Appl
28	557.5	22.8	216	15	US-10-250-553-19	Sequence 19, Appl
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30	549	22.7	448	14	US-10-340-779A-4	Sequence 4, Appli
31	548	22.7	454	14	US-10-369-493-6107	Sequence 6107, Ap
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37	522.5	21.6	448	15	US-10-702-777-5	Sequence 5, Appli
38	522.5	21.6	497	16	US-10-425-114-52563	Sequence 52563, A
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42	500.5	20.7	444	15	US-10-029-160-26	Sequence 26, Appl
43	498.5	20.6	444	15	US-10-239-652A-7	Sequence 7, Appli
44	498.5	20.6	473	15	US-10-239-652A-8	Sequence 8, Appli
45	494	20.5	432	14	US-10-191-513A-9	Sequence 9, Appli

ALIGNMENTS

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US-09-769-863-14
; Sequence 14, Application US/09769863
; Publication No. US2003015714A1
; GENERAL INFORMATION:
;  APPLICANT: Abbott Laboratories
;  APPLICANT: Mukerji, Pradip
;  APPLICANT: Huang, Yung-Sheng
;  APPLICANT: Das, Tapas
;  APPLICANT: Thurmond, Jennifer
;  APPLICANT: Pereira, Suzette L.
;  TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
;  FILE REFERENCE: 6763.US.O1
;  CURRENT APPLICATION NUMBER: US/09/769,863
;  CURRENT FILING DATE: 2001-01-25
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 14
;  LENGTH: 453
;  TYPE: PRT
;  ORGANISM: Saprolegnia diclina
US-09-769-863-14

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  Best Local Similarity   100.0%;
  Matches  453;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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OM protein - protein search, using sw model

                                 GenCore version 5.1.6
                                 Copyright (c) 1993 - 2005 Compugen Ltd.

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Perfect score:   2415
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Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters:   513545

Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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6	943	39.0	457	3	4	US-08-834-033A-14	Sequence 14, Appl
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9	943	39.0	457	4	4	US-09-377-452-4	Sequence 4, Appl
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11	943	39.0	458	4	4	US-09-439-261-44	Sequence 44, Appl
12	943	39.0	458	4	4	US-09-227-613-11	Sequence 11, Appl
13	943	39.0	458	4	4	US-09-227-613-41	Sequence 41, Appl
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16	775.5	32.1	355	3	4	US-09-363-574-5	Sequence 5, Appl
17	775.5	32.1	355	4	4	US-09-363-526-5	Sequence 5, Appl
18	713.5	29.5	323	4	4	US-09-439-261-17	Sequence 17, Appl
19	713.5	29.5	323	4	4	US-09-227-613-17	Sequence 17, Appl
20	644.5	26.7	421	4	4	US-09-857-583B-4	Sequence 4, Appl
21	586.5	24.3	443	4	4	US-09-857-583B-14	Sequence 14, Appl
22	561.5	23.3	447	4	4	US-09-857-583B-2	Sequence 2, Appl
23	535	22.2	452	3	4	US-08-934-254-27	Sequence 27, Appl
24	535	22.2	452	4	4	US-09-685-775-27	Sequence 27, Appl
25	527.5	21.8	448	4	4	US-09-857-583B-15	Sequence 15, Appl
26	526.5	21.8	446	2	4	US-08-833-610-5	Sequence 5, Appl
27	526.5	21.8	446	3	4	US-08-834-033A-15	Sequence 15, Appl
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ALIGNMENTS

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; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.01
; CURRENT APPLICATION NUMBER: US/09/769,863
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-09-769-863-14

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OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: May 27, 2005, 05:30:42 ; Search time 318 Seconds
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Title: US-10-054-534B-14
Perfect score: 2415
Sequence: 1 MVQGQKAEKISWATIREENR..........EVVVHLERISIEFFKEFPAM 453

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2415	100.0	453	6	AAE31900	Aae31900 Saprolegn
2	2415	100.0	453	8	ADR20163	Adr20163 Saprolegn
3	1537	63.6	459	8	AAE22063	Aae22063 Pythium i
4	1129.5	46.8	477	5	ABB98275	Abb98275 Phaeodact
5	1129.5	46.8	477	8	ABG73600	Abg73600 P. tricor
6	1129.5	46.8	477	8	ADR49338	Adr49338 Phaeodact
7	1129.5	46.8	477	8	ADR49342	Adr49342 Phaeodact
8	943	39.0	457	2	AAW84137	Aaw84137 A delta-6
9	943	39.0	457	2	AAW95504	Aaw95504 Mortierel
10	943	39.0	457	2	AAW85121	Aaw85121 A delta-6
11	943	39.0	457	3	AAY56045	Aay56045 Fungal de
12	943	39.0	457	3	AAY92599	Aay92599 M. alpina
13	943	39.0	457	4	AAB31684	Aab31684 Amino aci
14	943	39.0	457	8	ADR20161	Adr20161 Mortierel
15	943	39.0	458	5	ABG96527	Abg96527 M. alpina
16	943	39.0	458	5	ABG96509	Abg96509 M. alpina
17	943	39.0	458	5	ABG94707	Abg94707 Human del
18	943	39.0	458	5	ABG94693	Abg94693 Human del
19	943	33.9	467	6	ABB99479	Abb99479 Amino aci
20	817	33.8	520	4	AAB46440	Aab46440 C. purpur
21	817	33.1	483	4	AAB46436	Aab46436 C. purpur
22	798.5	33.1	483	4	AAB46435	Aab46435 C. purpur
23	775.5	32.1	355	4	AAW84139	Aaw84139 Desaturas
24	758	31.4	525	3	AAY51354	Aay51354 Protein b
25	758	31.4	525	4	AAB46810	Aab46810 P. patens
26	758	31.4	525	5	ABB98277	Abb98277 Physcomit
27	758	31.4	525	5	ABG73602	Abg73602 P. patens
28	758	31.4	525	5	ABG73607	Abg73607 P. patens
29	758	31.4	525	5	ABG73609	Abg73609 P. patens
30	758	31.4	525	8	ADR49326	Adr49326 Physcomit
31	758	31.4	525	8	ADR49315	Adr49315 Physcomit
32	713.5	29.5	323	5	ABG96515	Abg96515 M. alpina
33	713.5	29.5	323	8	ABG94698	Abg94698 Human del
34	631.5	26.1	421	8	ADP87981	Adp87981 Euglena g
35	619.5	25.7	422	3	AAY96722	Aay96722 E. gracil
36	585.5	24.2	443	2	AAY17751	Aay17751 Caenorhab
37	571	23.6	462	3	AAY51552	Aay51552 Corn sphi
38	567.5	23.5	473	3	AAY51353	Aay51353 Protein b
39	567.5	23.5	473	8	ADN23455	Adn23455 Bacterial
40	565	23.4	515	8	ADJ48443	Adj48443 Maize oil
41	561.5	23.3	447	2	AAY21891	Aay21891 C. elegan
42	561.5	23.3	447	3	AAY96721	Aay96721 C. elegan
43	561.5	23.3	447	8	ADP87987	Adp87987 Ceratodon
44	558.5	23.1	458	3	AAY51348	Aay51348 Sphingoli
45	558.5	23.1	458	7	ADF69394	Adf69394 Cytochrom

ALIGNMENTS

RESULT 1
AAE31900
ID   AAE31900 standard; protein; 453 AA.
XX
AC   AAE31900
XX
DT   07-MAR-2003 (first entry)
XX
DE   Saprolegnia diclina delta 6 desaturase.
XX
KW   Delta 5 desaturase; delta 6 desaturase; polyunsaturated fatty acid; PUFA;
KW   angioplasty; osteoporosis; inflammation; rheumatoid arthritis; psoriasis;
KW   premenstrual syndrome; myalgic encephalitis; chronic fatigue; vasotropic;
KW   acquired immune deficiency syndrome; AIDS; multiple sclerosis; virucide;
KW   osteopathic; litholytic; nephrotropic; neuroprotective; anticoagulant;
KW   therapy; antilipaemic; hypotensive; kidney stone; cachexia; cytostatic;
KW   eczema; cancer; asthma; enzyme.
XX
OS   Saprolegnia diclina.
XX
PN   WO200281668-A2.
XX
PD   17-OCT-2002.
XX
PF   24-JAN-2002; 2002WO-US001924.
XX
PR   25-JAN-2001; 2001US-00769863.
PR   22-JAN-2002; 2002US-00054534.
XX
PA   (ABBO) ABBOTT LAB.
XX
PI   Mukerji P, Huang Y, Das T, Thurmond J, Pereira SL;
XX
DR   WPI; 2003-067519/06.
DR   N-PSDB; AAD49064.
XX
PT   New delta 5 desaturase or delta 6 desaturase polypeptides, useful for
PT   producing polyunsaturated fatty acids, desaturates polyunsaturated fatty
PT   acids at carbon 5 and carbon 6, respectively.
XX
PS   Example 2; Page 148-149; 165pp; English.
XX
CC   The invention relates to delta 5 desaturase or delta 6 desaturase
CC   polypeptides and their nucleic acids. These sequences are useful for
CC   producing polyunsaturated fatty acids (PUFA) by desaturating PUFA at
CC   carbon 5 and carbon 6. Composition comprising at least one PUFA is useful
CC   for preventing or treating a condition caused by insufficient intake of
CC   PUFA. It is useful for treating restenosis after angioplasty, symptoms of

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OM nucleic - nucleic search, using sw model

                        Copyright (c) 1993 - 2005 Compugen Ltd.
                                                          GenCore version 5.1.6

Run on:           May 27, 2005, 00:44:37 ; Search time 8715 Seconds
                                                           (without alignments)
                                                           5948.771 Million cell updates/sec

Title:            US-10-054-534B-13
Perfect score:    1362
Sequence:         1 atggtccaggggcaaaaggc.........aggagttcccgccatcgtaa 1362
Scoring table:    IDENTITY NUC
                  - Gapop 10.0 , Gapext 1.0
Searched:         34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters:        68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        EST:*
                  1:    gb_est1:*
                  2:    gb_est2:*
                  3:    gb_htc:*
                  4:    gb_est3:*
                  5:    gb_est4:*
                  6:    gb_est5:*
                  7:    gb_est6:*
                  8:    gb_gss1:*
                  9:    gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                     SUMMARIES

Result                %
No.    Score   Query Match Length DB    ID           Description
-----  -----   -----------------  --    --           -----------
   1      96     7.0      819      5     BU745135     BU745135 CH1#007_D
c  2    93.6     6.9      458      7     CN006019     CN006019 ip37f09.g
c  3    93.6     6.9      600      7     CK999942     CK999942 ip37f09.b
c  4     93      6.8      390      4     AW052655     AW052655 rs38a08.y
   5    92.8     6.8      509      4     BG608740     BG608740 307418 MA
   6    92.6     6.8      884      5     BQ881930     BQ881930 AGENCOURT
   7     92      6.8      614      5     BP161817     BP161817 AGENCOURT
   8    91.4     6.7      421      7     CF140245     CF140245 UI-HF-CB0
c  9    91.4     6.7      530      2     AW246354     AW246354 2822200.5
c 10    91.4     6.7      535      2     BF207014     BF207014 60197O487
c 11    91.4     6.7      581      5     BP252288     BP252288 BP252288
c 12    91.4     6.7      581      5     BP255845     BP255845 BP255845
  13    91.4     6.7      582      5     BP254298     BP254298 BP254298
  14    91.4     6.7      585      5     BP242668     BP242668 BP242668
  15    91.4     6.7      598      7     CN283566     CN283566 170004245
  16    91.4     6.7      629      4     BG390559     BG390559 60241633O
c 17    91.4     6.7      633      2     BE313171     BE313171 60114992B
c 18    91.4     6.7      641      2     BE382648     BE382648 601297091
  19    91.4     6.7      666      4     CD618242     CD618242 56061114H
  20    91.4     6.7      689      4     BG696921     BG696921 60256868B
c 21    91.4     6.7      693      5     BU623713     BU623713 UI-H-FG1-
c 22    91.4     6.7      730      5     BU626230     BU626230 UI-H-FG1-
c 23    91.4     6.7      753      4     BG422898     BG422898 60245O074
  24    91.4     6.7      754      4     BG696675     BG696675 602658982
c 25    91.4     6.7      783      4     BG743255     BG743255 602633329
  26    91.4     6.7      799      4     BG743597     BG743597 602633951
c 27    91.4     6.7      815      5     BX440551     BX440551 BX440551
  28    91.4     6.7      830      4     BG674961     BG674961 602621157
  29    91.4     6.7      830      4     BG742494     BG742494 602633324
c 30    91.4     6.7      840      5     BU195643     BU195643 AGENCOURT
  31    91.4     6.7      841      5     BQ423614     BQ423614 AGENCOURT
c 32    91.4     6.7      882      5     BQ229517     BQ229517 AGENCOURT
c 33    91.4     6.7      892      6     CA488914     CA488914 AGENCOURT
c 34    91.4     6.7      892      6     CA488914     CA488914 AGENCOURT
c 35    91.4     6.7      895      6     BG743088     BG743088 602634223
  36    91.4     6.7      903      5     BQ721408     BQ721408 602620919
  37    91.4     6.7      894      6     CA487874     CA487874 AGENCOURT
  38    91.4     6.7      908      5     BU527215     BU527215 AGENCOURT
  39    91.4     6.7      922      5     BU156232     BU156232 AGENCOURT
  40    91.4     6.7      935      4     BG420045     BG420045 602453732
  41    91.4     6.7      983      4     BI199054     BI199054 602759167
  42    91.4     6.7     1167      4     BM478399     BM478399 AGENCOURT
  43    91.4     6.7     1335      4     AY418548     AY418548 Homo sapi
c 44    91.2     6.7      489      2     AW231075     AW231075 uo70e04.y
c 45    91.2     6.7      834      5     BX455254     BX455254 BX455254
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```
                                     ALIGNMENTS

RESULT 1
BU745135/c
LOCUS       BU745135                 819 bp    mRNA    linear    EST 10-OCT-2002
DEFINITION  CH1#007 D09T3 Canine heart non-normalized cDNA library in
            pBluescript Canis familiaris cDNA clone CH1#007_D09 3', mRNA
            sequence.
ACCESSION   BU745135
VERSION     BU745135.1    GI:23694297
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 819)
  AUTHORS   Yi,Y., Desai,R., Olatte,M., Henthorn,P. and George A.L.
  TITLE     Expressed sequence tags from Canine heart
  JOURNAL   Unpublished (2003)
COMMENT     Other ESTs: CH1#007_D09T7
            Contact: George AL
            Division of Genetic Medicine
            Vanderbilt University
            529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
            Tel: 615 936 2660
            Fax: 615 936 2661
            Email: al.george@vanderbilt.edu
            Insert Length: 1655  Std Error: 0.00
            Seq primer: T3: ATTAACCCTCACTAAAGGGA
            High quality sequence start: 65
            High quality sequence stop: 628.
FEATURES             Location/Qualifiers
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                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /clone="CH1#007_D09"
                     /tissue_type="heart"
                     /cell_type="heart"
                     /dev_stage="mixed developmental stages (adult, 30 day - 40
                     day fetal)"
                     /clone_lib="Canine heart non-normalized cDNA Library in
                     pBluescript"
                     /note="Organ: heart; Vector: pBluescript; Site 1: 5' of
                     vector Noti; Site 2: 3' of vector EcoRI; Tissue source:
                     dog heart (adult, 30 day - 40 day fetal), right and left
                     atria and ventricle. Dog breed - mixed (beagle, German
                     shepherd, pointer, Irish setter). library construction:
                     oligo-dT primed"
```

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: May 27, 2005, 03:05:18 ; Search time 2408 Seconds
    (without alignments)
    3472.625 Million cell updates/sec

Title: US-10-054-534B-13
Perfect score: 1362
Sequence: 1 atggtccaggggcaaaaggc..........aggagttcccgccatgtaa 1362
Scoring table: IDENTITY NUC
  Gapop 10.0 , Gapext 1.0
Searched: 5700845 seqs, 3069779757 residues

Total number of hits satisfying chosen parameters: 11401690

Post-processing: Minimum Match 0%
  Maximum Match 100%
  Listing first 45 summaries

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Database :

Published_Applications NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1362	100.0	1362	16	US-10-054-534B-13	Sequence 13, Appl
3	1362	100.0	1362	17	US-10-431-952-13	Sequence 13, Appl
4	1362	100.0	1362	18	US-10-776-311-35	Sequence 35, Appl
5	641.6	100.0	1380	9	US-09-967-477B-7	Sequence 7, Appli
6	342.8	47.1	1434	17	US-10-250-821-3	Sequence 3, Appli
7	342.8	25.2	1434	17	US-10-250-553-3	Sequence 3, Appli
8	273.6	20.1	1374	18	US-10-840-478-25	Sequence 25, Appl
9	260.6	19.1	8894	19	US-10-840-325-124	Sequence 124, App
10	259.6	19.1	1374	16	US-10-278-391-3	Sequence 3, Appli
11	259.6	19.1	1374	18	US-10-840-478-1	Sequence 1, Appli
12	259.6	19.1	1374	19	US-10-840-325-36	Sequence 36, Appl
13	259.6	19.1	1617	18	US-10-776-311-33	Sequence 33, Appl
14	258	18.9	10328	19	US-10-840-325-129	Sequence 129, App
15	149.6	11.0	648	17	US-10-250-821-18	Sequence 18, Appl
16	149.6	11.0	648	17	US-10-250-553-18	Sequence 18, Appl
17	113.4	8.3	1095	15	US-10-156-761-2285	Sequence 2285, Ap
18	113.4	8.3	9025608	15	US-10-156-761-1	Sequence 1, Appli
19	107.2	7.9	2054	18	US-10-389-566-288	Sequence 288, App
20	106	7.8	1944	18	US-10-437-963-83761	Sequence 83761, A
21	91.4	6.7	1335	17	US-10-239-552A-4	Sequence 4, Appli
22	91.4	6.7	1474	19	US-09-925-298-232	Sequence 232, App
23	91.4	6.7	1474	14	US-10-102-806-232	Sequence 232, App
24	91.4	6.7	1575	17	US-10-264-237-670	Sequence 670, App
25	91.4	6.7	1686	15	US-10-191-513A-6	Sequence 6, Appli
26	91.4	6.7	1843	15	US-10-191-513A-7	Sequence 7, Appli
27	91.4	6.7	2257	15	US-10-191-513A-8	Sequence 8, Appli
28	91.4	6.7	2540	17	US-10-641-643-295	Sequence 295, App
29	91.4	6.7	3016	17	US-10-429-160-25	Sequence 25, Appl
30	91.4	6.7	3149	17	US-10-172-118-1010	Sequence 1010, Ap
31	91.4	6.7	3149	17	US-10-342-887-1010	Sequence 1010, Ap
32	91.4	6.7	3149	19	US-10-928-465-64	Sequence 64, Appl
33	89.6	9	883	19	US-09-823-245A-303	Sequence 303, App
34	89.6	6.6	1059	19	US-10-278-698-174	Sequence 174, App
35	89.6	6.6	1059	19	US-10-278-698-690	Sequence 690, App
36	89.6	6.6	1092	17	US-10-264-237-563	Sequence 563, App
37	89.6	6.6	1717	14	US-10-262-617-2	Sequence 2, Appli
38	89.6	6.6	1757	18	US-10-788-792-42	Sequence 42, Appl
39	89.6	6.6	1772	17	US-10-296-115-562	Sequence 562, App
40	89.6	6.6	1408	17	US-10-425-114-17460	Sequence 17460, A
41	89.2	6.5	1059	15	US-10-156-761-1580	Sequence 1580, Ap
42	87.4	6.4	347	9	US-09-796-692-4558	Sequence 4558, Ap
43	87.4	6.4	347	14	US-10-040-862-4558	Sequence 4558, Ap
44	87.4	6.4	347	17	US-10-057-475B-4558	Sequence 4558, Ap
45	87.4	6.4	347	17	US-10-154-884B-4558	Sequence 4558, Ap

ALIGNMENTS

RESULT 1
US-09-769-863-13

Sequence 13, Application US/09769863
Publication No. US20030157144A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763.US.O1
CURRENT APPLICATION NUMBER: US/09/769,863
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1362
TYPE: DNA
ORGANISM: Saprolegnia diclina
US-09-769-863-13

Query Match 100.0%; Score 1362; DB 10; Length 1362;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTCCAGGGGCAAAAGGCCGGAGAAGAGATCTCGTGTGGGCGACCATCCGTGAGCACCGC 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 ATGGTCCAGGGGCAAAAGGCCGGAGAAGAGATCTCGTGTGGGCGACCATCCGTGAGCACCGC 60

Qy 61 CAAGACAACGCGGTGGATCGTGATCCACCACAAGGTGTACGACATCTCGGGCCTTTGAGGAC 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 CAAGACAACGCGGTGGATCGTGATCCACCACAAGGTGTACGACATCTCGGGCCTTTGAGGAC 120

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: May 27, 2005, 00:54:26 ; Search time 264 Seconds
(without alignments)
8441.700 Million cell updates/sec

Title: US-10-054-534B-13
Perfect score: 1362
Sequence: 1 atggtccaggggcaaaagc.........aggagttccgcgccatgtaa 1362

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81818359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :
  Issued_Patents_NA:*
  1: /cgn2_6/ptcdata/1/ina/5A_COMB.seq:*
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  3: /cgn2_6/ptcdata/1/ina/6A_COMB.seq:*
  4: /cgn2_6/ptcdata/1/ina/6B_COMB.seq:*
  5: /cgn2_6/ptcdata/1/ina/PCTUS_COMB.seq:*
  6: /cgn2_6/ptcdata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1362	100.0	1362	4	US-09-769-863-13	Sequence 13, Appl
2	259.6	19.1	1617	2	US-08-834-655-1	Sequence 1, Appli
3	259.6	19.1	1617	3	US-08-834-033A-1	Sequence 1, Appli
4	259.6	19.1	1617	3	US-09-363-574-1	Sequence 1, Appli
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16	89.6	6.6	1717	4	US-09-048-888-2	Sequence 2, Appli
17	89.6	6.6	1758	4	US-09-949-016-4904	Sequence 4904, Ap
18	89.6	6.3	347	4	US-09-702-705-355	Sequence 355, App
19	85.8	6.3	347	4	US-09-736-457-355	Sequence 355, App
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25	77.6	5.7	1478	4	US-09-148-545-63	Sequence 63, Appl
26	70.2	5.2	1320	4	US-09-769-863-28	Sequence 28, Appl
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			2277	2	US-08-098-487-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-769-863-13
Sequence 13, Application US/09769863
Patent No. 6635451
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.01
; CURRENT APPLICATION NUMBER: US/09/769,863
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Saprolegnia diclina
US-09-769-863-13

Query Match   100.0%; Score 1362; DB 4; Length 1362;
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Qy 241 CAGTCGACGCGGCGGCCCGTCGACACGTCGATCCTCGGACACGAAGCCAGTCGGAC 300
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OM nucleic - nucleic search, using sw model

                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:             May 26, 2005, 23:08:41 ; Search time 820 Seconds
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Scoring table:      IDENTITY NUC
                    Gapop 10.0 ; Gapext 1.0
Searched:           4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters:    8780412

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Post-processing:    Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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2	1362	100.0	1362	13	ADR20162	Adr20162 Saprolegn
3	641.6	47.1	1380	6	AAD35090	Aad35090 Pythium i
4	342.8	25.2	1434	6	ABV74258	Abv74258 Phaeodact
5	342.8	25.2	1434	6	ABQ76780	Abq76780 P. tricor
6	342.8	25.2	1443	13	ADR49337	Adr49337 Phaeodact
7	342.8	17061	17061	13	ADR49339	Adr49339 Plasmid p
8	259.6	19.1	1374	2	AAZ47129	Aaz47129 Fungal de
9	259.6	19.1	1617	3	AAV63624	Aav63624 cDNA enco
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12	259.6	19.1	1617	12	ADF89958	Adf89958 M. alpina
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17	129	9.5	1404	8	ABV76916	Abv76916 Nucleotid
18	107.2	7.9	2054	12	ADJ48284	Adj48284 Maize oil
19	106.2	7.8	2160	4	AAF25734	Aaf25734 C. purpur
20	100.6	7.4	1275	3	AAA51233	Aaa51233 E. gracil

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ALIGNMENTS

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XX
DT   07-MAR-2003  (first entry)
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DE   Saprolegnia diclina delta 6 desaturase DNA.
XX
KW   Delta 5 desaturase; delta 6 desaturase; polyunsaturated fatty acid; PUFA;
KW   angioplasty; osteoporosis; inflammation; rheumatoid arthritis; psoriasis;
KW   premenstrual syndrome; myalgic encephalitis; chronic fatigue; vasotropic;
KW   acquired immune deficiency syndrome; AIDS; multiple sclerosis; virucide;
KW   osteopathic; litholytic; nephrotropic; neuroprotective; anticoagulant;
KW   therapy; antilipaemic; hypotensive; kidney stone; cachexia; cytostatic;
KW   eczema; cancer; asthma; enzyme; gene; ds.
OS   Saprolegnia diclina.
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PN   WO200281668-A2.
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PD   17-OCT-2002.
XX
PF   24-JAN-2002; 2002WO-US001924.
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PR   25-JAN-2001; 2001US-00769863.
PR   22-JAN-2002; 2002US-00054534.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Mukerji P, Huang Y, Das T, Thurmond J, Pereira SL;
XX
DR   WPI; 2003-067519/06.
DR   P-PSDB; AAD49064.
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PT   New delta 5 desaturase or delta 6 desaturase polypeptides, useful for
PT   producing polyunsaturated fatty acids, desaturates polyunsaturated fatty
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26	91.4	6.7	1474	3	AAF21845	Aaf21845 Human bre
27	91.4	6.7	1575	6	ABL90108	Abl90108 Human pol
28	91.4	6.7	1686	2	AAV63641	Aav63641 Contig 25
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: May 27, 2005, 00:04:07 ; Search time 6176 Seconds
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Searched: 4708233 seqs, 2422767955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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24	253.2	18.6	1374	8	AF465282	Mortierel
25	248.4	18.2	1374	8	AF465281	Mortierel
26	246.8	18.1	1374	8	AF307940	Mortierel
27	245.6	18.0	1374	8	AF306634	Mortierel
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29	213.8	15.7	1521	8	AB070555	Mortierel
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ALIGNMENTS

RESULT 1
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LOCUS	AR410195	1362 bp	DNA	linear	PAT 18-DEC-2003

DEFINITION Sequence 13 from patent US 6635451.
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VERSION   AR410195.1   GI:40161436
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1362)
  AUTHORS   Mukerji,P., Huang,Y.-S., Das,T., Thurmond,J. and Pereira,S.L.
  TITLE   Desaturase genes and uses thereof
  JOURNAL   Patent: US 6635451-A 13 21-OCT-2003;
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ORIGIN

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